

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 7, 2002, 16:03:52 ; Search time 180.87 Seconds  
(without alignments)  
44.479 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307  
Sequence: 1 CELYRMSTYSTFPAGVPVSE.....KVKCFCCGLMDNKKLDSP 55

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORNITHINE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	301	98.0	1140	4 Q9UNH1	Q9unh1 homo sapien
2	298	97.1	602	1 Q9ESE9	Q9ese9 rattus norv
3	291	94.8	589	11 Q9QZC6	Q9qzc6 rattus norv
4	291	94.8	589	11 Q9ESE8	Q9ese8 rattus norv
5	247	80.5	324	13 Q9PDN2	Q9pdn2 gallus gall
6	247	80.5	610	13 Q57319	Q57319 gallus gall
7	152	49.5	436	11 Q9ESFO	Q9esfo rattus norv
8	152	49.5	501	11 Q9EQ05	Q9eq05 rattus norv
9	152	49.5	501	11 Q9EQ04	Q9eq04 rattus norv
10	145	47.2	264	12 Q9EN27	Q9en27 amasaca moo
11	143	46.6	195	13 Q9IA70	Q9ia70 gallus gall
12	143	46.6	197	13 Q9IA69	Q9ia69 gallus gall
13	140	45.6	281	12 Q9YNL8	Q9ynl8 choristomeu
14	134	43.6	397	11 Q9R015	Q9r015 mus musculu
15	131	42.7	224	11 Q9R015	Q9r015 mus musculu
16	127	41.4	438	5 Q9VUX5	Q9vux5 drosophila
17	119	38.8	208	12 Q55770	Q55770 chillo iride
18	117	38.1	280	4 Q9HAP7	Q9hap7 homo sapien
19	117	38.1	298	4 Q9H2A8	Q9h2a8 homo sapien

20	113.5	37.0	153	5 Q9VEM2	Q9vem2 drosophila
21	111	36.2	313	12 Q9J827	Q9j827 spodioptera
22	107	34.9	379	5 Q9U492	Q9u492 trichoptera
23	106	34.5	377	5 Q9NJ07	Q9nj07 spodioptera
24	105.5	34.4	276	12 Q89744	Q89744 buzura supp
25	103	33.6	150	12 Q9YVJ4	Q9yvJ4 melanoplus
26	103	33.6	261	13 Q9QES9	Q9qes9 epiphyas po
27	101	32.9	268	12 Q9E232	Q9e232 helioverpa
28	100	32.6	268	12 Q9IF18	Q9if18 helioverpa
29	92	30.0	301	12 Q9P254	Q9p254 trichoplusi
30	90	29.3	281	12 Q9DVT5	Q9dvt5 pluteilla xy
31	88	28.7	87	11 Q9Y119	Q9y119 mus musculu
32	87	28.3	285	12 Q9PYO9	Q9py09 xestia c-ni
33	86.5	28.2	292	12 Q9Z394	Q9z394 bombyx mori
34	84	27.4	87	11 Q9J123	Q9j123 mus musculu
35	84	27.4	87	11 Q9J120	Q9j120 mus musculu
36	83.5	27.2	187	12 Q9DSW8	Q9dsw8 ascovirus d
37	82	26.7	155	12 Q9YMI9	Q9ymi9 lymantria d
38	77.5	25.2	284	12 Q9YKL5	Q9ykl5 epiphyas po
39	73.5	23.9	137	4 Q9BVZ4	Q9bvz4 homo sapien
40	72.5	23.6	142	6 Q9GLN5	Q9gln5 sus scrofa
41	71.5	23.3	4845	11 Q88738	Q88738 mus musculu
42	69.5	22.6	4904	5 Q9VH01	Q9vh01 drosophila
43	69	22.5	250	12 Q99GV5	Q99gv5 helioverp
44	68	22.1	428	12 Q99GM7	Q99gm7 helioverp
45	65.5	21.3	234	12 Q9YMP8	Q9ymp8 lymantria d

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT: 1140 AA.
Q9UNH1	Q9UNH1:	Q9UNH1:	
AC	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	API2-MLT FUSION PROTEIN.		
GN	API2-MLT.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9272400; PubMed=10339464;		
RA	Dierlamm J., Baens M., Wlodarska I., Stefanova-Ouzounova M.,		
RA	Hernandez J.M., Hossfeld D.K., De Wolf-Peeters C., Hagemeijer A.,		
RA	Van den Berghe H., Marynen P.;		
RT	*The apoptosis inhibitor gene API2 and a novel 18q gene, MLT, are		
RT	recurrently rearranged in the t(11;18)(q21;q21)p66associated with		
RT	mucosa-associated lymphoid tissue lymphomas.*;		
RL	Blood 93:3601-3609(1993).		
CC	-I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
CC	DOMAIN.		
CC	EMBL: AF123094; AADA6161.1; .		
DR	HSSP: Q13490; IOBH.		
DR	InterPro: IPR001370; BIR.		
DR	InterPro: IPR003576; Caspase.		
DR	InterPro: IPR001309; ICE_P20.		
DR	InterPro: IPR003598; IG_c2.		
DR	InterPro: IPR003600; IG_1like.		
DR	InterPro: IPR003006; IG_MHC.		
DR	pfam: PF00653; BIR; 3.		
DR	SMART: SM00238; BIR; 2.		
DR	SMART: SM00115; CASc; 1.		
DR	SMART: SM00408; IGc2; 1.		
DR	SMART: SM00410; IG_1like; 1.		
DR	PROSITE: PS01282; BIR_REPEAT_1; 3.		
DR	PROSITE: PS50143; BIR_REPEAT_2; 3.		
DR	PROSITE: PS50208; CASPASE_P20; 1.		

SO SEQUENCE 1140 AA: 128738 MW: 0C18D890287C723E CRC64:

Query Match 98.0%; Score 301; DB 4; Length 1140;

Best Local Similarity 98.2%; Pred. No. 5, 6e-30;

Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CELYRMSTYSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGLMDNMKLGDSP 55  
 |||||||  
 Db 28 CELYRMSTYSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGLMDNMKRGDSP 82

RESULT 2

ID Q9ES9 PRELIMINARY; PRT; 602 AA.

AC Q9ES9;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INHIBITOR OF APOPTOSIS PROTEIN 1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI\_TaxID=10116;

RP [1]

RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

RT Cloning and Characterization of the Rat Homologs of the Inhibitor of

Apoptosis Protein 1, 2, and 3 Genes."

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

DR EMBL; AF183430; AAG22970.1; -

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR pfam; PF00653; BIR; 3.

DR pfam; PF00619; CARD; 1.

DR pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE; PS50209; CARD; 1.

DR Zinc-finger.

KW ZINC-FINGER.

SO SEQUENCE 602 AA: 67326 MW: CC91385EA62DE5A CRC64;

Query Match 97.1%; Score 298; DB 11; Length 602;

Best Local Similarity 96.4%; Pred. No. 6, 9e-30;

Matches 53; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CELYRMSTYSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGLMDNMKLGDSP 55  
 |||||||  
 Db 28 CELYRMSTYSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGLMDNMKRGDSP 82

RESULT 3

ID Q9QZC6 PRELIMINARY; PRT; 589 AA.

AC Q9QZC6;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INHIBITOR OF APOPTOSIS PROTEIN 2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI\_TaxID=10116;

RP [1]

RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

RT Cloning and Characterization of the Rat Homologs of the Inhibitor of

Apoptosis Protein 1, 2, and 3 Genes."

RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2.;"

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

DR EMBL; AF190020; AAF04585.1; -

DR HSSP; Q13490; 1QBH.

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR pfam; PF00653; BIR; 3.

DR pfam; PF00619; CARD; 1.

DR pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.

DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE; PS50209; CARD; 1.

DR Zinc-finger.

KW ZINC-FINGER.

SO SEQUENCE 589 AA: 66777 MW: E6812FEE3EA34142 CRC64;

Query Match 94.8%; Score 291; DB 11; Length 589;

Best Local Similarity 94.5%; Pred. No. 5, 3e-29;

Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CELYRMSTYSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGLMDNMKLGDSP 55  
 |||||||  
 Db 24 CELYRMSTYSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGLMDNMKRGDSP 78

RESULT 4

ID Q9ES8 PRELIMINARY; PRT; 589 AA.

AC Q9ES8;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INHIBITOR OF APOPTOSIS PROTEIN 2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI\_TaxID=10116;

RP [1]

RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

RT Cloning and Characterization of the Rat Homologs of the Inhibitor of

Apoptosis Protein 1, 2, and 3 Genes."

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

DR EMBL; AF183431; AAG22971.1; -

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR pfam; PF00653; BIR; 3.

DR pfam; PF00619; CARD; 1.

DR pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00238; BIR; 3.

DR SMART; SM00114; CARD; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE; PS50209; CARD; 1.

DR Zinc-finger.

KW ZINC-FINGER.

SO SEQUENCE 589 AA: 66750 MW: B4F7089BD7CD285B CRC64;

Query Match 94.8%; Score 291; DB 11; Length 589;

Best Local Similarity 94.5%; Pred. No. 5, 3e-29;

Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CELYRMSTYSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGLMDNMKLGDSP 55  
 |||||||  
 Db 24 CELYRMSTYSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGLMDNMKRGDSP 78



Db 26 EFNRLKTFANFPSSSPVSASTLARAGFLYTGGDTVOCFSCHAAVDWMQYGD 78

RESULT 8 PRELIMINARY: PRT: 501 AA.

09EQ05: 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE INHIBITOR OF APOPTOSIS PROTEIN 3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WISTAR: TISSUE-OVARY.

RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;

RT "Cloning, characterization and regulation of an inhibitor of apoptosis

protein in the rat corpus luteum."

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

DR EMBL: AF304333; AAG41192.1; -

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001841; znf\_ring.

DR Pfam: PF00653; BIR: 3.

DR SMART: SM00238; BIR: 3.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.

DR ZINC-finger.

SO SEQUENCE 501 AA; 56548 MW; 0973PFB28E81C5A0 CRC64;

Query Match 49.5%; Score 152; DB 11; Length 501;

Best Local Similarity 50.9%; Pred. No. 2.8e-11;

Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 2 ELYMSTYTFPAGVYSESLARAGFYTYGVNDVKYKFCGGLMDWKKLGD 54

Db 26 EFNRLKTFANFPSSSPVSASTLARAGFLYTGGDTVOCFSCHAAVDWMQYGD 78

RESULT 9 PRELIMINARY: PRT: 501 AA.

09EQ04: 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE INHIBITOR OF APOPTOSIS PROTEIN 3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WISTAR: TISSUE-OVARY.

RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;

RT "Cloning, characterization and regulation of an inhibitor of apoptosis

protein in the rat corpus luteum."

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

DR EMBL: AF304334; AAG41193.1; -

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001841; znf\_ring.

DR Pfam: PF00653; BIR: 3.

DR Pfam: PF00097; zfc3HC4; 1.

DR SMART: SM00238; BIR: 3.

DR SMART: SM00184; RING: 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.

KW Zinc-finger.

SO SEQUENCE 501 AA; 56578 MW; 4863F69F2E0C8CD CRC64;

Query Match 49.5%; Score 152; DB 11; Length 501;

Best Local Similarity 50.9%; Pred. No. 2.8e-11;

Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 2 ELYMSTYTFPAGVYSESLARAGFYTYGVNDVKYKFCGGLMDWKKLGD 54

Db 26 EFNRLKTFANFPSSSPVSASTLARAGFLYTGGDTVOCFSCHAAVDWMQYGD 78

RESULT 10 PRELIMINARY: PRT: 264 AA.

09EN27: 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE AWV021.

GN AWV021.

OS Amsacta moorei entomopoxvirus (AmpV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;

OC Entomopoxvirus B.

OX NCBI\_TaxID=28321;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20396580; PubMed=10936094;

RA Bowden A.L., Glassberg K.J., Digians J., Shaw R., Farmerie W.,

RA Moyer R.W.;

RT "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:

Analysis and Comparison with Other Poxviruses."

RL Analysis and Comparison with Other Poxviruses."

RL Virology 274:120-139(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Bowden A.L., Glassberg K.J., Digians J., Shaw R., Farmerie W.,

RA Moyer R.W.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF250284; AAG02727.1; -

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001841; znf\_ring.

DR Pfam: PF00653; BIR: 2.

DR SMART: SM00238; BIR: 2.

DR SMART: SM00184; RING: 1.

DR PROSITE: PS0143; BIR\_REPEAT\_2; 2.

SO SEQUENCE 264 AA; 30547 MW; 2EB72DA4B58D920A CRC64;

Query Match 47.2%; Score 145; DB 12; Length 264;

Best Local Similarity 49.0%; Pred. No. 1.1e-10;

Matches 25; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 5 RMSTYTFPAGVYSESLARAGFYTYGVNDVKYKFCGGLMDWKKLGDSP 55

Db 110 RUKTYKEMPISPISTEKLAEGFFYTGSKDKVCFYCDGLNKEWEDDP 160

RESULT 11 PRELIMINARY: PRT: 195 AA.

09IA70: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE INHIBITOR OF APOPTOSIS 1 (FRAGMENT).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OX NCBI\_TaxID=9031;

RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-BRED LEGHORN; TISSUE=SPLEEN;
RA Zhou H., Lamont S.J.;
RT *Genetic variation among chicken lines and mammalian species in
RT specific genes.*;
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF221082; AAF35319.1; -.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT 195
SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match
Best Local Similarity 46.6%; Score 143; DB 13; Length 195;
Best Local Similarity 51.0%; Pred. No. 1.5e-10;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 5 RMSTYTFPAGVPSERSLARAGFYTGVDKVCPCCGMLDMWKLGSDP 55
D 119 RVKTFINMPRIPOEQLADAGFYVGRNDVKCFCCDGLRCWESGDDP 169
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 12
Q91A69 PRELIMINARY; PRT; 197 AA.
AC Q91A69;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS 1 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRED FAYOUMI; TISSUE=SPLEEN;
RA Zhou H., Lamont S.J.;
RT *Genetic variation among chicken lines and mammalian species in
RT specific genes.*;
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF221083; AAF35320.1; -.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT 197
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match
Best Local Similarity 46.6%; Score 143; DB 13; Length 197;
Best Local Similarity 51.0%; Pred. No. 1.5e-10;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 5 RMSTYTFPAGVPSERSLARAGFYTGVDKVCPCCGMLDMWKLGSDP 55
D 120 RVKTFINMPRIPOEQLADAGFYVGRNDVKCFCCDGLRCWESGDDP 170
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 13
Q9YNL8 PRELIMINARY; PRT; 281 AA.
AC Q9YNL8;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

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DE IAP PROTEIN.
GN IAP.
OS Choriostoneura fumiferana nuclear polyhedrosis virus (CINPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10448;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IRELAND;
RA Lauzon H., Arif B.M., Ladd T., Palli R.;
RT *CINPV IAP gene.*;
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: U82510; AAD00537.1; -.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
KW Zinc-finger.
SQ SEQUENCE 281 AA; 32090 MW; B2D9BEA8A359F105E CRC64;

Query Match
Best Local Similarity 45.6%; Score 140; DB 12; Length 281;
Best Local Similarity 48.1%; Pred. No. 5.3e-10;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 2 ELYRSTYTFPAGVPSERSLARAGFYTGVDKVCPCCGMLDMWKLGSDP 55
D 124 EARLRTFTMPRGKQREKLAEGFFYTGSRDVKCFYCDGGLDMWEDDDEP 177
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 14
Q9R015 PRELIMINARY; PRT; 597 AA.
AC Q9R015;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE NEURONAL APOPTOSIS INHIBITOR PROTEIN.
GN BIRCle OR NAIp.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431676; PubMed=10501978;
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Nalp gene cluster on Chromosome 13 encodes several distinct
RT functional transcripts.*";
RL Mamm. Genome 10:1032-1035(1999).
DR EMBL: AF135493; AAD56765.1; -.
DR HSSP: Q13490; IQBH.
DR MCD: MGI:1298220; Bircle.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
SQ SEQUENCE 597 AA; 68322 MW; 4042E36E51A7F9A0 CRC64;

Query Match
Best Local Similarity 43.6%; Score 134; DB 11; Length 597;
Best Local Similarity 46.3%; Pred. No. 6.9e-09;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 2 ELYRSTYTFPAGVPSERSLARAGFYTGVDKVCPCCGMLDMWKLGSDP 55
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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